

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 8, 2002, 22:59:40 ; Search time 33.09 Seconds
(without alignments)
1042.825 Million cell updates/sec

Title: US-09-635-521a-2

Perfect score: 2334
Sequence: 1 MASPLPGSDCSQIDHSNV.....NSGAKPANSNAENGFOHEV 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

7 number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

PIR-68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	20.3	424	2 JH0164	neurotensin recept
2	466.5	20.0	418	2 S29506	neurotensin recept
3	419	18.0	416	2 S68822	hypothetical prote
4	303.5	13.0	378	2 T15816	angiotensin recept
5	272.5	11.7	380	2 I38435	endothelin recept
6	259.5	11.1	441	2 A41591	serotonin recept
7	256.5	11.0	564	2 A38271	somatostatin recept
8	252.5	10.8	428	2 S30508	probable G protein
9	250.5	10.7	428	2 A4021	somatostatin recept
10	250.5	10.7	428	2 S53336	galanin receptor 1
11	250.5	10.7	349	2 T53336	thyrotropin-releas
12	249.5	10.7	398	2 JN0708	endothelin recept
13	249.5	10.7	427	2 S13424	alpha-1A adreneryl
14	249.5	10.7	477	2 S71323	endothelin 1 and 2
15	248.5	10.6	426	2 A40440	galanin receptor -
16	248	10.6	394	2 JG7209	thyrotrophin-relea
17	247.5	10.6	411	2 I56444	thyroliberin recep
18	247.5	10.6	412	2 S23436	somatostatin recep
19	246.5	10.6	418	2 A62226	thyrotropin releas
20	245.5	10.5	352	2 JG0296	endothelin recept
21	245.5	10.5	427	2 A44158	somatostatin recep
22	244	10.5	391	2 A41795	somatostatin recep
23	244	10.5	381	2 C41795	somatostatin recep
24	244	10.5	391	2 A39297	thyrotropin-releas
25	243.5	10.4	393	2 A39251	cholecystokin re
26	242.5	10.4	444	2 A42685	hypothetical prote
27	242	10.3	425	2 J15959	kappa opioid recep
28	241.5	10.3	380	2 JG2338	mu opioid receptor
29	241	10.3	398	2 I56504	

30	241	10.3	398	2 I56517	mu opioid receptor
31	240	10.3	348	1 O080	rhodopsin - bovine
32	239.5	10.3	351	2 S29152	rhodopsin - chike
33	239	10.2	392	2 S65693	opioid receptor mu
34	239	10.2	400	2 I56553	mu opiate receptor
35	238.5	10.2	427	2 S50150	gastric CCK-A rece
36	238	10.2	355	2 A42347	opsin, green-sensl
37	238	10.2	387	2 S55550	5-HT4S receptor -
38	238	10.2	406	2 S55549	serotonin 4 recept
39	237.5	10.2	398	2 A57510	mu opioid receptor
40	237.5	10.2	442	1 JQ1042	endothelin recepto
41	237.5	10.2	466	2 S36794	beta-1-adrenerylc
42	236	10.1	348	1 S51677	rhodopsin - rat
43	236	10.1	418	1 GRHYB2	beta-2-adrenerylc
44	235.5	10.1	380	2 A55259	kappa opioid recep
45	235	10.1	363	2 I57955	somatostatin recep

ALIGNMENTS

RESULT 1	
JH0164	neurotensin receptor - rat
C:Species: Rattus norvegicus (Norway rat)	
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 17-Mar-2000	
C:Accession: JH0164	
R:Tanaka, K.; Masu, M.; Nakanishi, S.	
Neuron 4, 847-854, 1990	
A>Title: Structure and functional expression of the cloned rat neurotensin receptor.	
A:Reference number: JH0164; MUID:90297956	
A:Accession: JH0164	
A:Molecule type: mRNA	
A:Residues: 1-424 <TM>	
C:Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor. tter (neurotensin) binds in the brain and as a hormone) cellular mediator in peripheral t	
C:Superfamily: vertebrate rhodopsin	
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein	
F:65-87/Domain: transmembrane #status predicted <TM1>	
F:97-121/Domain: transmembrane #status predicted <TM2>	
F:144-165/Domain: transmembrane #status predicted <TM3>	
F:189-210/Domain: transmembrane #status predicted <TM4>	
F:236-260/Domain: transmembrane #status predicted <TM5>	
F:309-330/Domain: transmembrane #status predicted <TM6>	
F:348-372/Domain: transmembrane #status predicted <TM7>	
F:4,38,42/Binding site: carbohydrate (Asn) (covalent) #status predicted	
Query Match	20.3%; Score 473; DB 2; Length 424;
Best local Similarity	30.3%; Pred. No. 1.6e-33;
Matches 118; Conservative 67; Mismatches 161; Indels 44; Gaps 8;	
OY	30 KITLLIVYLIIFFVGLGNSATIRYQVLOKKGY--LQKVDHNVSLACSDIVFLGGM 87
DB	64 KVLVTAIYIALFVGTGVGNSVT--AFTLARKKSLOSLOSTVHYHGLSLASDLILLIAM 121
OY	88 PMEFYSIWNPLTSSVTLCKLHFLFACGSATLILHVLTSFERYIAICHPFYKAVS 147
DB	122 PVELYNITVHHNHWAGDACCRCGYFLRDACGYATRALNVASLSVERYLAIICHPFAKTLM 181
OY	148 GPQVKKLLIGFVWVTSALVALPILFLFAMGTEPYLVNVPSHRGILTCNRSSRHNEOETSNM 207
DB	182 SRSRTKKFISAIWLASALAIPLFLFMGLQ-----NRSGDGTI-----PGG 222
OY	208 SICITNLSRMT---VQSSIFGAFVYIVLVLSVAFMCMNMVQLM--KSQKSLA----- 258
DB	223 LVCPPIVDATFVAVIQTNTMSFLPMLVISTLNTVANKLTVAVYHQAABEGRICVGT 282
OY	259 -GGRPPQLKSSSEESRTARQTIIFRLIIVTLAVCMMPQRIKRIIMAAKPKDWTRS 317
DB	283 HNGEHSFTFWNITIEPGVQLLRGCVILRAVVAIFVVCMLPHVRLRMPCYISDQWTFE 342
OY	318 YFRAYMILPFSETFYLLSSVINPLLYTVSSQOFRRVYFQVQLCRSLDQAHNHRKRLRVH 377

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Db      1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
343 LEDEYHYEYMLTNALFEVSSANILTYLVNLSANRQVEYLTSLACLOCPGMRHRRKKR-----398
OY      378 AHSTDSARFYQRPDLFASRROSSARPTK 407
Db      399 -----PTFSRKPNSSMSNNHAFSTATRE 421

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RESULT 2

S29506
 neurensin receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence.Revision 13-Jan-1995 #text.change 17-Mar-2000
 C:Accession: S29506
 R:Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad, M.; Gully, D.; le F
 FEBS Lett. 317, 139-142, 1993
 A:Title: Cloning and expression of a complementary DNA encoding a high affinity human ne
 A:Reference number: S29506; MUID:93154505
 A:Accession: S29506
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1418 <VIT>
 A:Cross-references: EMBL:X70070; NID:g35020; PIDD:CAA49675.1; PID:g35021
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	20.0%;	Score 466.5;	DB 2;	Length 418;
Best Local Similarity	32.4%;	Pred. No. 5.7e-33;		
Matches 114;	Conservative 66;	Mismatches 137;	Indels 35;	Gaps 10

QY	22	EEFVAT--WIKITLILVYLFWGLGNSATFRVQYLOKKGY--LQEKVTHMVSILAC	77
Db	53	ELDVMTDILSKVILVAVYALFVGVYIGN--IYVATLTKRKSLOSLOSIVYHGLSLAL	110
QY	78	SDILVFLIGMPMEYSIIWNLDTTSSYLLCSKLHFLFECASYATLLVLTLSERYIAT	137
Db	111	SQLTLILLAMVELEYELNLTWHHMPAFEGDAGCCRQYFELRPACTYATALVASTLSERYIAT	170
QY	138	CHPFRKAWSPCCOVKLLIGFWVWTSALVATLPLTFEMAGTEYLVAVNPBSHGLTQNRBSRTR	197
Db	171	CHPFRKATLMSRSRKRKFTSALMLASALLVLPMLFTMGEO-----NRADG	216
QY	198	HHGEQFSNMSICR--NLSRRTVQSSILFCAGFVYLVYLLSVAFCQANMVOYLAK--S	252
Db	217	QH-----AGLIVCTPPTLHTLTVKVVIVQVNTVMSFELPRVIVSVLMTIANKLTVMVQAA	271
QY	253	OKGSL--AGGTRPOLKKSSEESERT--ARKOTIIELRILVTLVYALCWMPNDIRIRIMAAK	309
Db	272	EOGGVCTVGGGEH--STFSMAIEGGRVQALRHGVRVLRAVAVIAFVVCMLPVRVRLMHCYI	329
QY	310	PKHMDTRSYFRAYMILLPSEETFEYLSYINPLTLTVSSQOFRFRFVQYLC	361
Db	330	SDEQMTPLPIIFYHYFMVMTNALFVYSITINPLTLNLVSAENRHFLPATLAC	381

RESULT 3

S668822
 neurotensin receptor 2, levocabastine-sensitive - rat
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 20-Jun-2000
 C.Accession: S668822
 C.Citation: R.R.Chalon, P. Vitta, N. Kagnad, M. Guillemot, M. Bonnin, J. Delpech, B. le Fur, G.,
 FEBS Lett. 386, 91-94, 1996
 A.Title: Molecular cloning of a levocabastine-sensitive neurotensin binding site.
 A.Reference number: S668822; MUID:96228041
 A.Accession: S668822
 A.Molecule type: mRNA
 A.Residues: 1-416 <CH>
 A.Cross-references: GB:X97121; NID:g1483579; PIDN:CA65787.1; PID:g1483580
 A.Experimental source: hypothalamus
 C.Superfamily: vertebrate rhodopsin
 C.Keywords: G protein-coupled receptor; transmembrane protein

F:33-58/Domain	transmembrane	#status predicted	<TM1>
F:70-91/Domain	transmembrane	#status predicted	<TM2>
F:110-131/Domain	transmembrane	#status predicted	<TM3>
F:155-175/Domain	transmembrane	#status predicted	<TM4>
E:204-230/Domain	transmembrane	#status predicted	<TM5>
E:296-315/Domain	transmembrane	#status predicted	<TM6>
F:333-351/Domain	transmembrane	#status predicted	<TM7>

Query Match	18.0%;	Score 419;	DB 2;	Length 416;
Best Local Similarity	28.0%;	Pred. No. 7.8e-29;		
Matches 104;	Conservative 73;	Mismatches 145;	Indels 50;	Gaps 8

```

QY 28 WITLITLIVYLIFPMWGLLNSATIRVTOYLQKKGYLQKREVTMDHACSLDIFELIGM 87
Db 30 WAKVLETTALYSILTEFAFGTAGNLSNVH--YKAKAGRGPRGRHYHVLSTALSLSLIVSM 87
QY 88 PBEYSIINPLTTSSTYLSCKLHTFLFEACSVATLHVLTLSFEERYIACHPFRYKAVS 147
Db 88 PMLLYFWMSHPWFGDGLGCRGYTFYRELCAATAYLSVASLSAEGLCAVCPRLARLL 147
QY 148 GPCQVLLIGFWVTSAVALPRLFAMGTEYPLVNPVPSHRGILTKRKSSTRIHNEOPETSM 207
Db 148 TPRTTRRLSLVWVASLIDLAPMAVINGOKH---EVEADG-----BPEPAS- 191
QY 208 SICTNLSSWNY---FQSSIGGAVVLYLVLLVSALMCMNMAYL----- 249
Db 192 RCTVTVSATLQVLEFIQVNVLSFALPLATLARIITVNHMLAYSOVPSASQVSSIP 251
QY 250 ---MKQKG-----SLAGSTRPOLRKSESESTARQTIIFRLIYTVLAWC 296
Db 252 SRLELSEEGILLGFTTWKRTLSLQVQASLVRRHDAQIISLDHSAQV-LRAIVAYVICW 310
QY 297 MPNQIRIIMAAKPRHDTNRSYFRAYMILLPFSETEFFLSVINBLTVSSQQFRRFV 356
Db 311 LPYHARRLMYCYIPDDGWTINELDYFYHYFYMYNTLTFYSSAVPDIYNNAVSSSFRFL 370
QY 357 OYVLCRLSLQHA 368
Db 371 ESIGSLGGBQHS 382

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RESULT 4

T15816
hypothetical protein C48C5.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C:Accession: T15816
R:Ravello, A.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C48C5.
A:Reference number: Z18410
A:Accession: T15816
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-378 >FAV>
A:Cross-references: EMBL:U09994; NID:g1055102; PID:g1055105; PIDN:AAB37017.1; GSPDB:C.G5825
A:Experimental source: strain Bristol N2; clone C48C5
C:Genetics:
A:Gene: CESP.C48C5.1
A:Map position: X
A:Introns: 53/3; 87/2; 136/2; 169/3; 209/3; 231/3; 259/3; 286/1; 327/1
A:superfamily: adenosine receptor A1

Query Match	13.0%;	Score 303.5;	DB 2;	Length 378;
Best Local Similarity	26.28;	Pred. No. 8.2e-19;		
Matches 92; Conservative	66;	Mismatches 140;	Indels 53;	Gaps 14;

QY 27 TWIKITLILVYLIFVMGLGNSATIRTVQLRKGYLOKEVTDMWVSLACSDILVELIG 86
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 50 TLKVAAL-YIFELVGVI GNTT--CLVKKHHPMKKTTHASMTLMNLAVSDELVTLCVG 106

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OY      87 MPMEYSIINMPDLTSSVTLSCKLHTEFLFEACSAATLLHVLTLSFERIALCHP-ERKA 145
       :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db      105 LPFE-VMMNMNQYMPPEPDYICNLKALIAETTSVSITLIIIEIRVAACHPLFMKV 163
OY      146 VSGPCQVKLLIGFWNVASALVALPLLEFAMGETEPLVNPVSHRGILTCKNSSTRHHOPETS 205
       :| | | | :| | | | :| | | | :| | | | :| | | | :| | | | :| | | |
Db      164 QPFRRNIGTIIGFWIMISILCAMPFALHHRADYLKMSPG---TDNRIPVK-----SS 213
OY      206 NMSICT----NLSSRMTV--FOSSIFGAFVYLVVLVSLAFCMWMNQVLKMSQKSL 257
       :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      214 KCMIAVWFEPKLAFTFKLFHFSAIAFFALPLETIVLYLRAC-----KVSS 262
OY      258 AGGRHPOLRKSESESSTARQTIIIFRLIVTVLAVCMPMNQIRIMAAPKH---DW 314
Db      263 NRTIOPGEGLDITEELQMRIN-----AIICAIVSAFECICYLPFQLORLIFFEDNEVILTW 317
OY      315 TRSYFRAMILLPFSETEFFVLSVINPLLYTSSQOFRRVFQVL---CCR 362
Db      318 VNQM-T-FEI---SGLEFLYLATIINPIAYMLASSRFRAKKDLIDYCWR 362

R      5
C:Species: Homo sapiens (man)
C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 21-Jul-2000
C:Accession: I38435
R:B.O'Dowd, B.F.; Heibler, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petrij, T.
Gene 136, 355-360, 1993
A:Title: A human gene that shows identity with the gene encoding the angiotensin receptor
A:Reference number: I38435; MUID:94124031
A:Accession: I38435
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <RES>
A:Cross-references: EMBL:U03642; NID:g425351; PIDN:AAAI8954.1; PID:g425352
C:Genetics:
A:Gene: APJ
A:Map position: 11q12
A:introns: #status absent
C:Superfamily: vertebrate rhodopsin

Query Match          11.7%; Score 272.5; DB 2; Length 380;
Best Local Similarity 24.6%, Pred. No. 4,2e-16;
Matches 91; Conservative 62; Mismatches 154; Indels 63; Gaps 14;

OY      8 GSDSQIIDHSVPEFEVATWIKIILL-VYLIIFVNGLLGNSTATIRVQLQKKYIQ 65
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4 GGDFFNYAGADQSCECTDKMKSSGALLPAIYMVELLGTTGNGILV--WTVFRSREKR 61
OY      66 KEVDTHMYLASCDIIVLIGPMPEFYSIINPNLTSSY-----TLSCKLHTEFLFACS 120
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      62 RSADFIASLAADV-LTVVVTLF-----LMATYYRIORYDMPEGFGFPCKLSYLLFVMY 114
OY      121 ATULLHVLTLSFERIYAICHP-----ERYKAVSGPCQVKLLIGFWNTSVALTVALPLLEFMG 175
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      115 ASVFCLTGISFDRIYLAIRPVANARLRLR-VSGAVATAVL---WTLAALLAMPVM-VLDR 168
OY      176 TEYPLVNPVSHHGILTKNSSTRHHOPETSNNISICTNLSSRMT---YFOSSIFCAFVY 231
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      169 TTGGDENLTK---VQC-----YMDSMVAWYVSSSEAWMEVGGVSTVGFVPV 213
OY      232 LVLLISVAFMCNMNAQVLMKSQGSLAGTRPPOLRKSESESERFARROTIIFRLIYVT 291
       :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db      214 FTIMLTCTCFE-----AQTIAGHR-----KERIDGLKRRRLRSIIIVLYVT 256
OY      292 LAVCMNPQDIRIMAANKPKHDWTRSYPRAWYILLPFSETFEVLSVINPLLYTSSQOF 351
       :| | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      257 FALCMWPYHLVKTLYMLGSLTMPCDFLELMNIIPPCTCIASYNSCLNPFYAFEDPRF 316
OY      352 RRVFQVQLCC 361
       :| :| | | |

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Db      317 RQACTSMJCC 326
RESULT   6
A:1591
endothelin receptor B precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: A41591; A61251; A41184; S63513
R:Saito, Y.; Mizuno, T.; Itakura, M.; Suzuki, Y.; Ito, T.; Hagiwara, H.; Hirose, S.
U. Biol. Chem. 266, 23433-23437, 1991
A>Title: Primary structure of bovine endothelin Et-B receptor and identification of s
A:Reference number: A41591; MUID:92078223
A:Accession: A41591
A:Molecule type: mRNA
A:Residues: 1-441 <SAT>
A:Cross-references: GB:D90456; NID:g217553; PIDN:EBA14422.1; PID:g217554
R:Hagiwara, H.; Kozuka, M.; Sakaguchi, H.; Eguchi, S.; Ito, T.; Hirose, S.
J. Cardiovasc. Pharmacol. 17(Suppl.7), S117-S118, 1991
A>Title: Separation and purification of 34- and 52-kDa species of bovine lung endothe
A:Reference number: A61251; MUID:92219662
A:Accession: A61251
A:Molecule type: protein
A:Residues: 304-315;424-432 <HAG>
R.Kozuka, M.; Ito, T.; Hirose, S.; Lodhi, K.M.; Hagiwara, H.
U. Biol. Chem. 266, 16892-16896, 1991
A>Title: Purification and characterization of bovine lung endothelin receptor.
A:Reference number: A41184; MUID:91338493
A:Accession: A41184
A:Molecule type: protein
A:Residues: 124-127;'S',263-269;304-316;418-421;424-432 <KOZ>
R.Hick, S.; Heldmann, J.; Sosik, V.; Mueller-Esterl, W.; Godovac-Zimmermann, J.
Eur. J. Biochem. 234, 251-257, 1995
A>Title: Isolation of the endothelin B receptor from bovine lung. Structure, signal s
A:Reference number: S63513; MUID:96096746
A:Accession: S63513
A:Molecule type: protein
A:Residues: 1,'X',3-7,'X',9-10;25-35;36-42;73-78;79-87;284-290;291-296,'X',298 <HC>
A:Superfamily: endothelin receptor B
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:1-26/Domain: signal sequence #status experimental <SIG>
F:27-44/Product: endothelin receptor B #status experimental <MAT>
F:101-116/Domain: transmembrane #status predicted <TM1>
F:137-162/Domain: transmembrane #status predicted <TM2>
F:175-186/Domain: transmembrane #status predicted <TM3>
F:218-242/Domain: transmembrane #status predicted <TM4>
F:271-295/Domain: transmembrane #status predicted <TM5>
F:324-349/Domain: transmembrane #status predicted <TM6>
F:362-388/Domain: transmembrane #status predicted <TM7>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match          11.1%; Score 259.5; DB 2; Length 441;
Best Local Similarity 23.8%; Pred. No. 6,8e+15;
Matches    89; Conservative 76; Mismatches 156; Indels 53; Gaps 14;

        2 ASPSLP-GSDCSQIIDHSHP---EFVATWIKITLLIYLIIFFMGLIGNSATRIVQY 57
           |||:||||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db     68 ATPQIPRGGRMGAPRPPTPCDGPTEIKEFKFYINTVAQCILVFGLGIIGNSTLR--I 124
           |||:||||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|:
QY    58 LOKKGYLQKEVDHAWVASLDLIWLFLGMPPEFSYI---WNPLTSSYTSLCKLHTFL 114
           |||:||||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db    125 IYNKNCRMRGNPIILLASIALGDLLIIDIPINTYKLAKDM-PGVGE---MKLVPFPI 179
           |||:||||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|:
QY   115 PFCASYATLLHLTLTSFERXYIAICHPFRKYAVSGPOCYKLLIGFWWTSAVALPLEPAM 174
           |||:||||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db   180 QKASVGITYLSICALSIDRYRAVNASMRIKGIGPKWAELVELLVWVSYYLAVP--EAV 237
           |||:||||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|:
QY   175 GTREYLVNPVPSHRGLTCNRSSRRHHQPETSMSICTNLSSKWTFYQ-----SSLFGAF 229
           |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   238 GPD---IITSDHIG-----NKLRIICLLHPDKTAFMQFYRTAKCMWFDS 278
           |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY   230 VLYVLVLTSAFECMMMQVLMKSQKGSGLAGTRPPQLRKRSSEESRTARQRQIFIRLIIV 289

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Db 279 FYFCLPLATLALTYLTMTCEMLKRSKM-----OIALNDHKKOREVAKTVECL--V 328
 QY 290 VYLAVQWMMNQIRIRIM-AAAKPKHMDTRSYFRAYMILLDF-SETFEYLSVYNPLLYTYS 347
 Db 329 LVFALCWLPHLSRIKLTLTYDQHDRRCFELSLVLDYIGINNASLNSCINPLALYLV 388
 QY 348 SQQFRFVVOVLCC 361
 Db 389 SKRFKNCFKSCLOC 402

RESULT 7

A38271
 Serotonin receptor 7 - fruit fly (Drosophila melanogaster)
 N:Alternate names: 5-hydroxytryptamine receptor 7 (5-HT7)
 C:Species: Drosophila melanogaster
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
 C:Accession: A38271
 R:Cross: P.; Amlaiky, N.; Plassat, J.L.; Maroteaux, L.; Borrelli, E.; Hen, R.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8940-8944, 1990
 A:Title: Cloning and characterization of a Drosophila serotonin receptor that activates
 A:Reference number: A38271; MUID:91062395
 A:Accession: A38271
 A:Molecule type: mRNA
 A:Residues: 1-564 <WIT>
 A:Cross-references: GB:M55533
 A:Note: the authors translated the codon CWT for residue 213 as Ala, GTG for residue 215
 C:Genetics:
 A:Gene: FlyBase:5-HT7
 A:Cross-references: FlyBase:FBgn0004573
 C:Superfamily: octopamine receptor type I
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; phosphoprotein

Query Match 11.1%; Score 259.5; DB 2; Length 564;
 Best Local Similarity 21.1%; Pred. No. 9e-15;
 Matches 92; Conservative 76; Mismatches 145; Indels 123; Gaps 14;

QY 6 LPQSDSQIDHSHVPEFEVATWIKITLLIVLIFVGMGLGNSATIRVTVLQKKGYLQ 65
 Db 138 VPLSDPRLLEERFAGEFVLRPLTSIFSVILVILGTVGVVLCVAVCRK---LR 194
 QY 66 KEVTDHNSACSDILVFLGPMF-EYSIT--WN--PLTTSYTSCKLHFTLFACSY 120
 Db 195 RPNVYLIVSLALSDLCVALLVMPALLYLEKMGFPL-----CDIWSFDVLCOT 247
 QY 121 ATLLHVLTSFEERYIAICHPFRKAVSGPOVLLIGFWVTSALVALPLLFAMGTEYPL 180
 Db 248 ASILNLCASVDRLIATYKPLEYGVKRTPRRMVLCVYIWLAACTSLPPLILGNE--- 304
 QY 181 VNPVSHRGILCNRSSTRNHEOPEPTSNMISICTNLSSRWTFVQSSIFGAFVYLVLLSVAF 240
 Db 305 -----HEDEGQPICTVQONFA--YQIR--ATLSGFILPSVLMFVY 343
 QY 241 MCNNMQVLMKSK-----GSLAGSTRPPOLKSKSESRARQOTII--- 283
 Db 344 QIFRAARRIVLEEKRAQTHLQALNGSGSPSAQAPP-LGHTELASSGNGORHSSVGNYS 402
 QY 284 -----FLRLIYVT 291
 Db 403 LTYSTGGGLSSGGGALAGHSGGSGVSGTGLGSPHHKRIKROLAKEKASTTLGITMISA 462
 QY 292 LAVCMNPQIRIRIAAARPKHMDTRSYFRAYMILLDFSETFE--YLSVYNPLLYTYS 348
 Db 463 FYVGMWLP---FTLLALRP-----FEIMHVPASLSFLMLGIVANSLNIIYATIN 511
 QY 349 QQFRFVVOVLCCRLS 364
 Db 512 RDRFRKPFQDILYFRCS 527

RESULT 8

157940
 Somatostatin receptor 5 - rat
 N:Alternate names: somatostatin release-inhibiting factor subtype 28 receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Nov-1999
 C:Accession: 157940; 157949; S39244
 R:Cross: R.O.; Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
 Mol. Pharmacol. 44, 1278, 1993
 A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with p
 A:Reference number: 157940; MUID:93125499
 A:Accession: 157940
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-363 <OCA1>
 A:Cross-references: GB:I04535; NID:g409238; PIDN:AAAI7029.1; PID:g409239
 R:Cross: R.O.; Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
 Mol. Pharmacol. 44, 1278, 1993
 A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with p
 A:Reference number: 157949; MUID:94088493
 A:Accession: 157949
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 341-363 <OCA2>
 A:Cross-references: GB:S67370; NID:g455947; PIDN:AAI29371.1; PID:g455948
 A:Experimental source: pituitary
 R:Penetta, R.; Greenwood, M.; Patel, Y.C.
 submitted to the EMBL Data Library, August 1993
 A:Description: Correction of the nucleotide and amino acid sequence of the rat somato
 A:Reference number: S39244
 A:Accession: S39244
 A:Molecule type: mRNA
 A:Residues: 309-363 <PEN>
 A:Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
 C:Genetics:
 A:Gene: SSTR5
 C:Superfamily: vertebrate rhodopsin

Query Match 11.0%; Score 256.5; DB 2; Length 363;
 Best Local Similarity 28.2%; Pred. No. 9.9e-15;
 Matches 98; Conservative 54; Mismatches 109; Indels 87; Gaps 18;

QY 35 LVYLIIFWGLGNSATIRVTVLQKKGYLQKEVTD-HMVSILACSDILVFLGPMFEYS 93
 Db 42 VYLVLTCTVGLSGNLTLYVVRNAK---MKTYNTIILMAADV-LFWGLP----- 92
 QY 94 IINPLTTSYTL-----CKLHFLFACSYATLLHVLTSFEERYIAICHPFRYA 145
 Db 93 -----LATQNAVSYWPGSFLCRLVMTLDGINOPTSIFCLMWSVDXYLAVHPLRSAR 147
 QY 146 VSGPOVKILIGFWVTSALVALPLLFAMGTEYPLVNPVSHRGILCNRSSTRNHEOPEPT 205
 Db 148 WRRPRVAKMASAAVWVFLSLMSLPDLV-----FADQDEGWS--TCNLS-----WPEPV 193
 QY 206 NMSICTNLSSRWTFVQSSIFGAFVYLVLL-----LSVAFCMNNMQVLMKSKSGSLAG 260
 Db 194 GL-----WG-----AAFTYTSVLGFFGLVYICLYLIVYKVR-----AAG 231
 QY 261 TRPPOLKSKSESESTRARQOTIIFRLIVTVLAV---CWNQOIRRI--MAAKPKHMDT 315
 Db 233 MRVGSRRRRSEPKYT-----RMVVVVVLFVFGCWLPEFIVNIYNLAFTLPEEPTS 282
 QY 316 RS-YFRAYMILLDFSETFEYLSVYNPLLYTVSSQOFRFVVOVLCCR 362
 Db 283 AGLYF--FVVVLS-----YANSCANPLLYGFLSDNFRQSRKYLCLR 322

RESULT 9

S30508
 probable G protein-coupled receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
 C:Accession: S30508

Db 141 RRSLSLRVSRNALLGVCIGWALISIMASPVAY-----HGGILF----- 177
 QY 201 QPETSMSICTLSSRMT-----VFQSSIFGAFVYVLLVLSVAMCMNMOMLKS 252
 Db 178 HPRASQPFQW---BQWDPDRHKKAYVCTFVEG---YLLPLLICICCYAKVNLHLKK 230
 QY 253 QKSLAGTRPPQLRKSESESRARQTIIFLRLLIYVTLAVCMNPNOIRIRMAAKPKH 312
 Db 231 LKN-----MSKSESKSKKKA--GTVL---VVVVVFGISWLPNHI-----IH 267
 QY 313 DWTSTFYAYMLLPSETF-----FYLSVYPLLYTSSQOFRRVVOYLCCRLSL 365
 Db 268 LWAE--FGVFP-LTPASFLFRITACLAAYSNSVNPDIYAFLESENRKAYKQVFKCH-- 322
 QY 366 QHANHEKRLRVHAHSTTDSARFVQRP 391
 Db 323 -----RKDSHLSDPKKNSRIIDPP 341

Respect 12

JN0708 thyrotropin-releasing hormone receptor - human

C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
 C:Accession: S40682; JN0759; S50151; S50152; I38356; JN0708
 R:Matre, V.; Karlens, H.E.; Wright, M.S.; Lundell, I.; Fjeldheim, A.K.; Gabrielsen, O.S.
 Biochem. Biophys. Res. Commun. 195, 179-185, 1993
 A:Title: Molecular cloning of a functional human thyrotropin-releasing hormone receptor.
 A:Reference number: S40682; MUID:93371401
 A:Accession: S40682
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-398 <MAT>
 A:Cross-references: EMBL:75071; NID:9404157; PIDN:CAA52965.1; PID:9404158
 R:Matada, M.; Monden, T.; Satoh, T.; Satoh, N.; Murakami, M.; Iriuchijima, T.; Kakegawa, K.
 Biochem. Biophys. Res. Commun. 195, 737-745, 1993
 A:Title: Pituitary adenomas of patients with acromegaly express thyrotropin-releasing hormone receptor gene.
 A:Reference number: JN0759; MUID:93384596
 A:Accession: JN0759
 A:Molecule type: mRNA
 A:Residues: 1-398 <YAM>
 A:Cross-references: GB:D16845; NID:9577631; PIDN:BA04120.1; PID:9577632
 R:Hinnma, S.; Hosoya, M.; Ogi, K.; Tanaka, H.; Nagai, Y.; Onda, H.
 Biochim. Biophys. Acta 1219, 251-259, 1994
 A:Title: Molecular cloning and functional expression of a human thyrotropin-releasing hormone receptor.
 A:Reference number: S50151; MUID:95002135
 A:Accession: S50151
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-263 <HIN>
 A:Accession: S50152
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 267-398 <H12>
 R:Duthie, S.M.; Taylor, P.L.; Anderson, L.; Cook, J.; Eidine, K.A.
 Mol. Cell. Endocrinol. 95, R11-R15, 1993
 A:Title: Cloning and functional characterisation of the human TRH receptor.
 A:Reference number: I38356; MUID:94063224
 A:Accession: I38356
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-398 <RES>
 A:Cross-references: EMBL:X72089; NID:9440155; PIDN:CAA50979.1; PID:9440156
 C:Genetics:
 A:Gene: GDB:TRHR
 A:Cross-references: GDB:228955; OMIM:188545
 A:Map position: 8q23-8q23
 C:Superfamily: adenosine receptor A1
 C:Keywords: G protein-coupled receptor; receptor; transmembrane protein
 F:29-51/Domain: transmembrane #status predicted <TM1>
 F:62-83/Domain: transmembrane #status predicted <TM2>

F:101-121/Domain: transmembrane #status predicted <TM3>
 F:146-168/Domain: transmembrane #status predicted <TM4>
 F:194-215/Domain: transmembrane #status predicted <TM5>
 F:267-288/Domain: transmembrane #status predicted <TM6>
 F:297-319/Domain: transmembrane #status predicted <TM7>

Query Match 10.7%; Score 249.5; DB 2; Length 398;
 Best Local Similarity 22.0%; Pred. No. 4, 5e-14;
 Matches 86; Conservative 69; Mismatches 119; Indels 117; Gaps 12;

QY 21 PEFVATWIKITLLVYLLIFVWGLGNSATIRVTOYLOKGYLOKEVTDHMYSLACSDI 80
 Db 16 PRAVALEYQVYVTLVLLICGLGIVGN---IMVLYVMTKTHKRPNTCYVLSVAVDL 72
 QY 81 LVFL-IGPMMEFYSIINNPPLTSSY-----TLCKLHTEFLFACSVATLLHVLTFSEF 133
 Db 73 MVLVAAGP-----NITDSIYGSWYGYVGCCTITLYQYLGINASSCSITAFIER 123
 QY 134 YIAICHPRIKAVSGPCQVKLLIGFVWVTSALVALPLLFAMGTETPLVNPFSHRG---LT 190
 Db 124 YIAICHPRIKQFLCTFSRAKIIIFVWAFSLCYCMWFLLD-----LNTSTYKDAIVIS 178
 QY 191 CNRSSTRHHEQPSNMSICTNLSSRMTVFQSSIFGAFVYVLLVLSVAPCMNMOMQVLM 250
 Db 179 CGYKISRMYSP-----IYLMDFGVYVYVPMILAVLV----- 211
 QY 251 KSKQSLAGTRPPQLRKSESESR-----ARQTIIF 284
 Db 212 -----GFIARILFLNPIDSPDENSKTWKNDSTHQNMLNVNTSNRCFNSVSSRKQYTKM 267
 QY 285 LRLVYVTLAVCMNPNOIRIRMAAKPKHDWTRTSFRAYML-----LPSETF----- 333
 Db 268 LAVVYVIFALMLP-----YRLVAVNSFLSPFQENWFLFCRI 307
 QY 334 --YLSVYVPLLYTSSQOFRRVVOYLCCR 362
 Db 308 CTVLSAIPVYVYVIMLSOKFAFRKILCNCK 338

RESULT 13

S13424 endothelin receptor - bovine
 C:Species: Bos primigenius laurus (cattle)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
 C:Accession: S13424
 R:Arai, H.; Hori, S.; Aramori, I.; Ohkubo, H.; Nakanishi, S.
 Nature 348, 730-732, 1990
 A:Title: Cloning and expression of a cDNA encoding an endothelin receptor.
 A:Reference number: S13424; MUID:91080923
 A:Accession: S13424
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-427 <ARA>
 A:Cross-references: GB:X57765; NID:9121; PIDN:CAA40917.1; PID:9122
 C:Superfamily: endothelin receptor B

Query Match 10.7%; Score 249.5; DB 2; Length 427;
 Best Local Similarity 23.2%; Pred. No. 4, 9e-14;
 Matches 92; Conservative 84; Mismatches 152; Indels 69; Gaps 19;

QY 17 HSHVP-EFEVATWIKITLLVYLLIFVWGLGNSATIRVTOYLOKGYLOKEVTDHMYSL 75
 Db 66 HNYCQOQRIKISAFKINVTYISCTFIYGVGNMNTLLRI--IYQNK-CMRGPNALIASL 122
 QY 76 ACSDLVFLKGMPEFYIIT---WNPPLTSSY-TLCKLHTEFLFACSVATLLHVLTLSEF 131
 Db 123 ALGDLIVYVIDLPINVEFKLLAGRW-PFEQNDGVEFLCKLFFELKSSVGITVLMCALSV 181
 QY 132 ERYVIAICHPRIKAVSGPCQVKLLIGFVWVTSALVALPLLFAMGTETPLVNP-----S 185
 Db 182 DTRAVASMSRVQIGIPLVYVIAIVLSIVLITLAIIP--EALG-----FVWVPEFYKGAQ 235

QY 186 HRLGTCNRSRHHHOPETSNMSICTNLSSRWTFVQSSIFGAFVYVLLISVAFMCMNM 245
 DB 236 HR--TCMLNAT-----SKMEFYQDYKDW-----LFGFY--FCMPLCTAIFPTLM 278
 QY 246 MQLVMSQKSLAGTRPPOLRKSESESRRTARRQTIIFRLIVTLAVCMMPNQIRRM 305
 DB 279 TCMLNRRNGSL-----RIALSEHLKOREVAKTFECL--VVIFALCMPELHLIRIL 328
 QY 306 -AAAKPKHDWTRSFRAVMILLPF-SEFFYLSVINPLTYVSSQOFRVAVOYLCC-- 361
 DB 329 KRYVYDEMKTNRCELLSPFLMDYIGINLATMNSCINPITALFYFSKFKKCFOSLCCCC 388
 QY 362 -----RLSLQHANHEKRLVHAHSTTDS 385
 DB 389 YQSKSLMTSVPMNGTSIQWKNEO-----NNHNTERRS 421

RESULT 14

S71323
 A:Title: adrenergic receptor - Japanese medaka
 C:Species: Oryzias latipes (Japanese medaka)
 C>Date: 23-Jul-1997 #sequence, revision 01-Aug-1997 #text_change 17-Mar-1999
 C:Accession: S71323
 R:Yasukoka, A.; Abe, K.; Arai, S.; Emori, Y.
 Eur. J. Biochem. 235, 501-507, 1996
 A:Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of M
 A:Reference number: S71323; MUID:96184522
 A:Accession: S71323
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-477 <YAS>
 A:Note: it is uncertain whether Met-1 or Met-8 is the initiator
 C:Superfamily: vertebrate rhodopsin

Query Match 10.7%; Score 249.5; DB 2; Length 477;

Best Local Similarity 20.9%; Pred. No. 5,5e-14; Matches 103; Conservative 85; Mismatches 146; Indels 159; Gaps 20;

QY 2 ASPSLPSGDCSQIIDSHVPEFEVAWIKITLLIVYLIFVWGLGNSATIRVTOYLQK 61
 DB 11 SSVVINCNSCHVL-----APELNTVKAVALGMVIGITLF--GVIGNILVI--LSVCHR- 62
 QY 62 GYLQKEVTDHVASLACSDILVFLIGMEFYSIINPLTSSY-TLSCKLHTLFECASY 120
 DB 63 -HLOTVTYFIVNLAVADLLSTVLP--FSALFEIIDRWVEGFRVCNIMAAVDVLCCT 118
 QY 121 ATLLHVLTLSPERTIACHPRKAYVSGPOVKLLIGFWWTSALVALPLLFAMGTREYPL 180
 DB 119 ASIMSICVIVDRITIGVYPLRPAIMTKRRALLAVMLLWLVSTIIGPLFGM----- 172
 QY 181 VNVDHRLGTCNRSRHHHOPETSNMSIC-TNLSSRWTFVQSSIFGAFVYVLLISV 239
 DB 173 -----KEPADEFVCKITPEPGYALF--SAVSFYFLPALILA-- 209
 QY 240 FMCNMAQVLYMSQKSLAGTRPPOLRKSESE-----ESTARRQTIIFL 285
 DB 210 -MYCRVYVVAOKESRGLKEG---QKLEKSDSEGVILRMHNGTIVSEDAISLRTFAL 264
 QY 286 RL-----IVTLAVCMMPNQIRIMAARAKKHMDTRSYFRAYMILLPF-- 328
 DB 265 RLKLFSSREKRAKTLGIVGCGVLCWLP-----FLVLDPDGS 301
 QY 329 -----SEFF-----YLSVINPLTYVSSQOFRVAVOYL--CCRLSLQHANHE 371
 DB 302 IFPAYRSDVFKITFLWLGFNSCINPITALFYFSKFKKCFOSLCCCC----- 354
 QY 372 KRLVHAHSTTDSARFQORPLLFASRQSSARREKIFLSTPQSEARPOSKSOSLSESL 431
 DB 355 --PRAHHH-----HLSVGOSQT--QCHSILTISLDSK 381

QY 432 EPNSGAKPANSAA 444
 DB 382 GAPCRISPSSSVA 394

RESULT 15

A04040
 A:Title: Endothelin 1 and 2 receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Jan-1993 #sequence, revision 22-Jan-1993 #text_change 16-Jul-1999
 C:Accession: A40440; B49197
 R:Lin, H.Y.; Kaji, E.H.; Winkler, G.R.; Ives, H.E.; Lodish, H.F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 3185-3189, 1991
 A:Title: Cloning and functional expression of a vascular smooth muscle endothelin 1 r
 A:Reference number: A40440; MUID:91195317
 A:Accession: A40440
 A:Molecule type: mRNA
 A:Residues: 1-426 <LIN>
 A:Cross-references: GB:M60786; NID:9204023; PID:AAA41114.1; PID:9204024
 R:Hori, S.; Komatsu, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
 Endocrinology 130, 1885-1895, 1992
 A:Title: Distinct tissue distribution and cellular localization of two messenger ribo
 A:Reference number: A49197; MUID:92191882
 A:Accession: B49197
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-45, 'N', 47-52, 'Q', 54-426 <HOR>
 A:Experimental source: lung
 A:Note: sequence extracted from NCBI backbone (NCBI:89467)
 C:Superfamily: endothelin receptor B
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-426/Product: endothelin 1 and 2 receptor #status predicted <MAT>

Query Match 10.6%; Score 248.5; DB 2; Length 426;

Best Local Similarity 23.5%; Pred. No. 5,9e-14; Matches 93; Conservative 78; Mismatches 160; Indels 65; Gaps 18;

QY 17 HSHVP-EFEVAWIKITLLIVYLIFVWGLGNSATIRVTOYLQKGYLQKEVTDHVASL 75
 DB 66 HGCPPOQTKITTFKXINVTISCTIPVGMVGNALTRI--IYQNK-CMRGSPNALIASL 122
 QY 76 ACSDILVFLIGMEFYSIINPLTSSY-TLSCKLHTLFECASYATLLHVLTSF 131
 DB 123 ALGDLIVYIDLPINVKLLAGRW-PEDHNDGVELCKLPFLQSSVGITVNLICALSV 181
 QY 132 ERYIACHPRKAYVSGPOVKLLIGFWWTSALVALPLLFAMGTREYPLVNP-----S 185
 DB 182 DRYRAVASMRVGGIIPDLTAELIVSILSLIALIP--EAIG-----FVMVPFEKGRQ 235
 QY 186 HRLGTCNRSRHHHOPETSNMSICTNLSSRWTFVQSSIFGAFVYVLLISVAFMCMNM 245
 DB 236 HR--TCMLNAT-----TKMEFYQDYKDW-----LFGFY--FCMPLCTAIFPTLM 278
 QY 246 MQLVMSQKSLAGTRPPOLRKSESESRRTARRQTIIFRLIVTLAVCMMPNQIRRM 305
 DB 279 TCMLNRRNGSL-----RIALSEHLKOREVAKTFECL--VVIFALCMPELHLIRIL 328
 QY 306 -AAAKPKHDWTRSYFRAYMILLPF-SEFFYLSVINPLTYVSSQOFRVAVOYLCC-- 361
 DB 329 KRYVYDEMCKNRCELLSPFLMDYIGINLATMNSCINPITALFYFSKFKKCFOSLCCCC 388
 QY 362 -----RLSLQHANHEKRLVHAHSTTDS 384
 DB 389 HOSKSLMTSVPMNGTSIQWKNEOHNHNTERRSSHKDS 424

Search completed: January 8, 2002, 23:07:48
 Job time: 488 sec

